

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 10, 2004, 04:46:06 ; Search time 37 Seconds
(without alignments)
522.430 Million cell updates/sec

Title: US-09-988-974-5

Sequence: 1 MAGKSLFKVILLGSGVGK.....LIQDTVNLHKKPKSSSCC 201

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR_76: *
1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

RESULT 1
G02361
small GTP binding protein Rab9 - human

C/Species: Homo sapiens (man)

C/Date: 06-Dec-1994 #sequence_revision 06-Jun-1997 #text_change 02-Feb-2001

C/Accession: G02361

R/Author: Y.A.; Davies, J.P.
submitted to the EMBL Data Library, December 1995

A/Reference number: H01115

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-201 <10A>

A/Cross-references: EMBL:U44103; NID:g1174146; PIDN:AA051200.1; PID:g1174147

C/Superfamily: ras transforming protein; translation elongation factor Tu homology

C/Keywords: GTP binding; nucleotide binding; P-loop

F/8-127/Domain: translation elongation factor Tu homology <ETU>

F/14-21/Region: nucleotide-binding motif A (P-loop)

F/124-127/Region: GTP-binding NKXD motif

F/154-156/Region: GTP-binding SAK/L motif

Query Match 100.0%; Score 1062; DB 2; Length 201;
Best Local Similarity 100.0%; Pred. No. 1.6e-89;
Matches 201; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGKSLFKVILLGSGVGKSLMNRVYTNKPDQLFHTIGVPLNKDLEVDGHPVTMOI 60

Db 1 MAGKSLFKVILLGSGVGKSLMNRVYTNKPDQLFHTIGVPLNKDLEVDGHPVTMOI 60

QY 61 WDTAGQERFRSLRTPPYRSGDCCLLTFSYDSSQSFNLNMWKEFIYADVPESESFPV 120

Db 61 WDTAGQERFRSLRTPPYRSGDCCLLTFSYDSSQSFNLNMWKEFIYADVPESESFPV 120

QY 121 ILGNKIDISERQVSTEAQAWCRDNGDYPYFESADATNVAAAFEAARVILATEDRSD 180

Db 121 ILGNKIDISERQVSTEAQAWCRDNGDYPYFESADATNVAAAFEAARVILATEDRSD 180

QY 181 HLIGDTVNLHKKPKSSSCC 201

Db 181 HLIGDTVNLHKKPKSSSCC 201

RESULT 2
S36187
GTP-binding protein rab9 - dog

C/Species: Canis lupus familiaris (dog)

C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 02-Feb-2001

C/Accession: S36187; C36364; S15605; S37290

R/Lombardi, D.; Soldati, T.; Riederer, M.A.; Gada, Y.; Zerial, M.; Pfeiffer, S.R.

EMBL:U44103; NID:g1174146; PIDN:AA051200.1; PID:g1174147

A/Title: Rab9 functions in transport between late endosomes and the trans Golgi network.

A/Reference number: S36187; M01D:93178443; PMID:8440258

QY	4 J
Db	5 J
QY	
Db	
QY	
Db	
QY	
Db	

RESUI
B3041
GTP-E
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C;Dat
C;Acc
R;Cha
Mol

A;Tit
A;Ref
A;Acc
A;Sta

A; Mol
A; Res
A; Cro
R; Cha

Cell	
A; Tit	
A; Ref	
A; Acc	

A; Stat
A; Mole
A; Resi
A; Cros

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58
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elli, R.

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OM protein - protein search, using sw model

Run on: February 10, 2004, 04:46:06 ; Search time 37 Seconds
(without alignments)
522.430 Million cell updates/sec

Title: US-09-988-974-5
Perfect score: 1062
Sequence: 1 MAGKSSLFKVLILGDGVGK.....LIQTDVNLHRKPKSSSCC 201

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database 1: PIR 76: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1062	100.0	201	G02361	small GTP binding
2	1057	99.5	201	S36187	GTP-binding protei
3	533	50.2	206	JC4107	membrane vesicle t
4	529	49.8	207	B30413	GTP-binding protei
5	529	49.8	207	JC5268	GTPase Rab7 protei
6	527	49.6	207	S62733	small GTP-binding
7	526.5	49.6	201	S01934	GTP-binding protei
8	523.5	49.3	205	S36368	GTP-binding protei
9	523	49.2	206	S33531	GTP-binding protei
10	520.5	49.0	207	T12579	GTP-binding protei
11	518.5	48.8	209	T26119	hypothetical protei
12	515	48.5	205	T03629	GTP-binding protei
13	514	48.4	205	T40425	ras-related protei
14	514	48.4	206	T03628	GTP-binding protei
15	509	47.9	206	H96562	hypothetical protei
16	501.5	47.2	206	C96529	probable RAB7 GTP-
17	499.5	47.0	206	S39566	rab7 protein - soy
18	499	47.0	203	T00770	GTP-binding protei
19	498	46.9	204	T03630	GTP-binding protei
20	496.5	46.8	206	S39567	rab7 protein - mot
21	495	46.6	208	A44334	GTP-binding protei
22	493	46.4	208	T04019	rab7 protein homol
23	484.5	45.6	230	C44606	probable RAS type
24	373	35.1	216	JN0056	GTP-binding protei
25	373	35.1	216	S36364	GTP-binding protei
26	373	35.1	216	S47169	GTP-binding protei
27	369.5	34.8	216	JC4108	GTP-binding protei
28	368	34.7	214	S10026	GTP-binding protei
29	359.5	33.9	202	S38740	GTP-binding protei

30	353	33.2	221	2	H71444	GTP-binding protei
31	352.5	33.2	203	2	S34253	GTP-binding protei
32	350	32.0	214	2	J50641	GTP-binding protei
33	349	32.9	218	2	C38625	GTP-binding protei
34	348	32.8	217	2	A86230	hypothetical protei
35	347	32.7	219	2	G84723	probable RAS type
36	346	32.6	218	2	JC2487	GTP-binding protei
37	346	32.6	218	2	A55005	GTP-binding protei
38	345	32.5	215	2	T06443	GTP-binding protei
39	344.5	32.4	217	2	S36365	GTP-binding protei
40	344	32.4	208	2	A38202	GTP-binding protei
41	343	32.3	202	2	S41430	GTP-binding protei
42	343	32.3	214	2	T14566	GTP-binding protei
43	341	32.1	211	2	T29035	hypothetical protei
44	341	32.1	223	2	S42679	GTP-binding protei
45	340.5	32.1	258	2	B86153	ARA-5 [imported] -

ALIGNMENTS

RESULT 1

G02361
small GTP binding protein Rab9 - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 02-Feb-2001
C:Accession: G02361
R.Ioannou, Y.A.; Davies, J.P.
submitted to the EMBL Data Library, December 1995
A:Reference number: H01115
A:Accession: G02361
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-201 <ICA>
A:Cross-references: EMBL:U44103; NID:g1174146; PIDN:AC51200.1; PID:g1174147
C:Superfamily: ras transforming protein; translation elongation factor Tu homology
C:Keywords: GTP binding; nucleotide binding; P-loop
F:8-127/Domain: translation elongation factor Tu homology <ETU>
F:14-21/Region: nucleotide-binding motif A (P-loop)
F:124-127/Region: GTP-binding NKXD motif
F:154-156/Region: GTP-binding SAK/L motif

Query Match		100.0%;	Score 1062;	DB 2;	Length 201;
Best Local Similarity		100.0%;	Pred. No. 1.6e-89;		
Matches 201;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MAGKSSLFKVLILGDGVGKSSLMNRVTYTNKFDLTQLEHTIGVEFLNKDLEVDGHFVTMQI	60		
DB	1	MAGKSSLFKVLILGDGVGKSSLMNRVTYTNKFDLTQLEHTIGVEFLNKDLEVDGHFVTMQI	60		
QY	61	WDTAGQERFSLRTPFYRGSDCCLLTFSDVDSQFQNLNKKKEFIYADVKEPESPPFV	120		
DB	61	WDTAGQERFSLRTPFYRGSDCCLLTFSDVDSQFQNLNKKKEFIYADVKEPESPPFV	120		
QY	121	ILGNKIDISERQVSTEAQWCRDNGDYPYFESAKDATNVAAPFAEAVRRVLATEDRSD	180		
DB	121	ILGNKIDISERQVSTEAQWCRDNGDYPYFESAKDATNVAAPFAEAVRRVLATEDRSD	180		
QY	181	HLIQTDTVNLHRKPKSSSCC	201		
DB	181	HLIQTDTVNLHRKPKSSSCC	201		

RESULT 2

S36187
GTP-binding protein rab9 - dog
C:Species: Canis lupus familiaris (dog)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 02-Feb-2001
C:Accession: S36187; S36364; S36365; S37290
R.Ioannou, Y.A.; Davies, J.P.
submitted to the EMBL Data Library, December 1995
A:Reference number: H01115
A:Accession: S36187; S36364; S36365; S37290
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-201 <ICA>
A:Cross-references: EMBL:U44103; NID:g1174146; PIDN:AC51200.1; PID:g1174147
C:Superfamily: ras transforming protein; translation elongation factor Tu homology
C:Keywords: GTP binding; nucleotide binding; P-loop
F:8-127/Domain: translation elongation factor Tu homology <ETU>
F:14-21/Region: nucleotide-binding motif A (P-loop)
F:124-127/Region: GTP-binding NKXD motif
F:154-156/Region: GTP-binding SAK/L motif

A:Accession: S36187

A:Molecule type: mRNA

A:Residues: 1-201 <LOM>

A:Cross-references: EMBL:X56386

R:Chavrier, P.; Vingron, M.; Sander, C.; Simons, K.; Zerial, M.

Mol. Cell. Biol. 10, 6578-6585, 1990

A:Title: Molecular cloning of YPT1/SEC4-related cDNAs from an epithelial cell line.

A:Reference number: A36364; MUID:91061765; PMID:2123294

A:Accession: C36364

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 30-201 <CHA>

A:Cross-references: GB:X56386; NID:g2189; PIDN:CAA39797.1; PID:g2190

C:Genetics:

A:Gene: rab9

C:Superfamily: ras transforming protein; translation elongation factor Tu homology

C:Keywords: GTP binding; nucleotide binding; P-loop

F:8-127/Domain: translation elongation factor Tu homology <ETU>

F:14-21/Region: nucleotide-binding motif A (P-loop)

F:124-127/Region: GTP-binding NKXD motif

F:154-156/Region: GTP-binding SAK/L motif

Query Match

Best Local Similarity 99.5%; Score 1057; DB 2; Length 201;

Matches 200; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGKSLFKVILLGSGVCKSLMNRVYTNKFDTLFHTIGVEFLNKDLEVDGHFTVMTQI 60

Db 1 MAGKSLFKVILLGSGVCKSLMNRVYTNKFDTLFHTIGVEFLNKDLEVDGHFTVMTQI 60

QY 61 WTAQGERFRSLRTPFYRGSDCLLTFSVDDSQSFQNLNNKKKEFIYADVKEPSPFFV 120

Db 61 WTAQGERFRSLRTPFYRGSDCLLTFSVDDSQSFQNLNNKKKEFIYADVKEPSPFFV 120

QY 121 ILGNKIDISERQVSTEEAQAQRCDNGDYPYFETSADATNVAAPEEAVRVLATERSD 180

Db 121 ILGNKIDISERQVSTEEAQAQRCDNGDYPYFETSADATNVAAPEEAVRVLATERSD 180

QY 181 HLIQTDVNLHKKPKPSSCC 201

Db 181 HLIQTDVNLHKKPKPSSCC 201

RESULT 3

A:Accession: J4107

R:Dietmaier, W.; Fabry, S.; Huber, H.; Schmitt, R.

Gene 158, 41-50, 1995

A:Title: Analysis of a family of ypt genes and their products from Chlamydomonas reinhardtii

N:Alternate names: ras-like yptC5 protein; small G protein yptC5

C:Species: Chlamydomonas reinhardtii

C:Date: 21-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 02-Feb-2001

A:Reference number: JCA105; MUID:95309723; PMID:7789809

A:Accession: JCA107

A:Molecule type: mRNA

A:Residues: 1-206 <DIE>

A:Cross-references: GB:U13170; NID:9806725; PIDN:AAA82728.1; PID:g806726

C:Comment: This protein plays an essential role in the regulation of intracellular membrane vesicle transport protein ypt C5 - Chlamydomonas reinhardtii

C:Genetics:

A:Gene: yptC5

A:Introns: 18/1; 60/3; 109/3; 136/3; 185/1

C:Superfamily: ras transforming protein; translation elongation factor Tu homology

C:Keywords: GTP binding; nucleotide binding; P-loop

F:9-128/Domain: translation elongation factor Tu homology <ETU>

F:15-22/Region: nucleotide-binding motif A (P-loop)

F:37-45/Domain: effector #status predicted <EPF>

F:125-128/Region: GTP-binding NKXD motif

F:158-160/Region: GTP-binding SAK/L motif

Query Match

Best Local Similarity 50.2%; Score 533; DB 2; Length 206;

Matches 105; Conservative 33; Mismatches 59; Indels 6; Gaps 3;

QY 4 KSSLFKVILLGSGVCKSLMNRVYTNKFDTLFHTIGVEFLNKDLEVDGHFTVMTQIWD 63

Db 5 KXRLLVIIIGSGVCKSLMNRVYTNKFDTLFHTIGVEFLNKDLEVDGHFTVMTQIWD 64

QY 64 AGQERFRSLRTPFYRGSDCLLTFSVDDSQSFQNLNNKKKEFIYADVKEPSPFFVILG 123

Db 65 AGQERFQSLGSAFYRGADCCVLVFDVNNNAKSPDDLDNRDEFIIQAGPPDPNFFPVLG 124

QY 124 NKIDI---SERQVSTEEAQAQRCDNGDYPYFETSADATNVAAPEEAVRVLATERSD 180

Db 125 NKIDENGSGSRQVSEKAKAWKSGKSPYFETSADATNVAAPEEAVRVLATERSD 183

QY 181 HLIQTDVNLH--RKPSPSSCC 201

Db 184 ELFMPPDAVDMNTTATQKRAQCC 206

RESULT 4

GTP-binding protein rab7 - dog

C:Species: Canis lupus familiaris (dog)

C:Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 02-Feb-2001

C:Accession: B30413; C39648

R:Chavrier, P.; Vingron, M.; Sander, C.; Simons, K.; Zerial, M.

Mol. Cell. Biol. 10, 6578-6585, 1990

A:Title: Molecular cloning of YPT1/SEC4-related cDNAs from an epithelial cell line.

A:Reference number: A36364; MUID:91061765; PMID:2123294

A:Accession: B30413

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-207 <CHA>

A:Cross-references: GB:M35522; NID:g164057; PIDN:AAA30890.1; PID:g164058

R:Chavrier, P.; Parton, R.G.; Hauri, H.P.; Simons, K.; Zerial, M.

Cell 62, 317-329, 1990

A:Title: Localization of low molecular weight GTP binding proteins to exocytic and endocytic

A:Reference number: A3648; MUID:90322428; PMID:2115402

A:Accession: C39648

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-207 <CH2>

A:Cross-references: GB:M35522; NID:g164057; PIDN:AAA30890.1; PID:g164058

C:Superfamily: ras transforming protein; translation elongation factor Tu homology

C:Keywords: GTP binding; membrane trafficking; nucleotide binding; P-loop

F:9-128/Domain: translation elongation factor Tu homology <ETU>

F:15-22/Region: nucleotide-binding motif A (P-loop)

F:125-128/Region: GTP-binding NKXD motif

F:155-157/Region: GTP-binding SAK/L motif

Query Match

Best Local Similarity 49.8%; Score 529; DB 2; Length 207;

Matches 98; Conservative 24; Mismatches 51; Indels 0; Gaps 0;

QY 4 KSSLFKVILLGSGVCKSLMNRVYTNKFDTLFHTIGVEFLNKDLEVDGHFTVMTQIWD 63

Db 5 KXRLLVIIIGSGVCKSLMNRVYTNKFDTLFHTIGVEFLNKDLEVDGHFTVMTQIWD 64

QY 64 AGQERFRSLRTPFYRGSDCLLTFSVDDSQSFQNLNNKKKEFIYADVKEPSPFFVILG 123

Db 65 AGQERFQSLGSAFYRGADCCVLVFDVNNNAKSPDDLDNRDEFIIQAGPPDPNFFPVLG 124

QY 124 NKIDISERQVSTEEAQAQRCDNGDYPYFETSADATNVAAPEEAVRVLATERSD 176

Db 125 NKIDLENRQVATKRAQAWCYKNNIPYFETSADATNVAAPEEAVRVLATERSD 177

RESULT 5

JCA3268

CTPase Rab7 protein - human

C:Species: Homo sapiens (man)

C:Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 02-Feb-2001

C:Accession: JCA3268

R:Vitelli, R.; Chiarlillo, M.; Lattero, D.; Bruni, C.B.; Buccì, C.

RESULT 7

S01934

Query Match 49.6%; Score 526.5; DB 2; Length 201;
Best Local Similarity 50.5%; Pred. No. 1.2e-40;
Matches 100; Conservative 32; Mismatches 63; Indels 3; Gaps 1;

N;Alternate names: ras transforming protein, 23K - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 02-Feb-2001
C;Accession: S01934
R;Buccia, C.; Frunzio, R.; Chiarotti, L.; Brown, A.L.; Rechler, M.M.; Bruni, C.B.
Nucleic Acids Res. 16, 9979-9993, 1988
A;Title: A new member of the ras gene superfamily identified in a rat liver cell line.
A;Reference number: S01934; MUID:89057527; PMID:3057452
A;Accession: S01934
A;Molecule type: mRNA
A;Residues: 1-201 <BUC>
A;Cross-references: EMBL:X12535
C;Superfamily: ras transforming protein; translation elongation factor Tu homology
C;Keywords: GTP binding; membrane trafficking; nucleotide binding; P-loop
F;3-122/Domain: translation elongation factor Tu homology <ETU>
F;9-16/Region: nucleotide-binding motif A (P-loop)
F;119-122/Region: GTP binding NXD motif
F;149-151/Region: GTP-binding SAK/L motif

QY 7 LFKVILLGDGVGKSSLMNRYVYNKFTQLPHTLIGVZFLNKLDEVDGHFVTMQIWDITAGQ 66
DB 2 LLKVIILGDGVGKTSLMNQYVANKKFSNQYKATIGADFLTKEVMVDRLVTMQIWDITAGQ 61
QY 67 ERFSLRTPPYRGSDCCLLTFSDDSQFNLNWKKEFTYYADVKEPSPFPFVILGNKI 126
DB 62 ERQSLGVAYRGADCCVLVFDVTAPNFTKLSWRDEFLIQASPRPENPFVVLGNKI 121
QY 127 DISERQVSTEEAQMCKNDGNGYFFETSAKADTNVAAAFEEAVRRVLAETE---DRSDHLI 183
DB 122 DLENRQVATKRAQWCYCKNNIPYFETSAKEAINVEQAFQTIARNALKQETVELYNEFP 181
QY 184 QTDVTNLHRKPKPSSSCC 201
DB 182 EPKLDKNERAKASASC 199

RESULT 8

S36368

Query Match 49.3%; Score 523.5; DB 2; Length 205;
Best Local Similarity 50.5%; Pred. NO. 2.2e-40;
Matches 102; Conservative 34; Mismatches 61; Indels 5; Gaps 3;

N;Alternate names: ras transforming protein; translation elongation factor Tu homology
C;Species: Volvox carteri
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 02-Feb-2001
C;Accession: S36368
R;Fabry, S.; Jacobsen, A.; Huber, H.; Palme, K.; Schmitt, R.
Curr. Genet. 24, 223-240, 1993
A;Title: Structure, expression, and phylogenetic relationships of a family of ypt genes
A;Reference number: S36365; MUID:94037148; PMID:8221932
A;Accession: S36368
A;Molecule type: DNA
A;Residues: 1-205 <FAB>
A;Cross-references: GB:L08131; NID:G409167; PIDN:AAA34254.1; PID:G409168
C;Genetics:
A;Gene: YptV5
A;Introns: 18/2; 60/3; 109/3; 135/3; 184/2
C;Superfamily: ras transforming protein; translation elongation factor Tu homology
C;Keywords: GTP binding; nucleotide binding; P-loop
F;9-128/Domain: translation elongation factor Tu homology <ETU>
F;15-22/Region: nucleotide-binding motif A (P-loop)
F;61-67/Region: GTP binding #status predicted
F;122-129/Region: GTP binding #status predicted
F;150-156/Region: GTP binding #status predicted

QY 4 KSLRFVILLGDGVGKSSLMNRYVYNKFTQLPHTLIGVZFLNKLDEVDGHFVTMQIWDIT 63

Db 5 KRVLVKIIILGDSGVGKTSIMNQYVQKFTKEYKATIGADFLTKIEVDKDKVTMQIWD 64
 QY 64 AGQERFSLRTPYRGSDCCLLTFSVDDSQFNLNKKKEFIYADVKEPESPFFVILG 123
 Db 65 AGQERFQSLGSAFYRGADCCMLVFDVNNNAKSFDDLDNRDEFILQAGSPDPPNFVVLG 124
 QY 124 NKIDI--SERQVSTEEAQAACRNDGDPYFETSAKDNTNVAAPFEAVRRVLATEDRSDH 181
 Db 125 NKIDVGNVRQVTEKKAKAWCAKSGSIPYFETSAKEDINVEAFTCIETNALRNE-KEEE 183
 QY 182 LIQTDTVNLHRK--PKPSSSC 201
 Db 184 LFPDPAVDMNTSATQRKGGCC 205

RESULT 9

S33531
 C:Superfamily: ras transforming protein rab - garden pea
 C:Species: Pisum sativum (garden pea)
 C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 02-Feb-2001
 C:Accession: S33531; S25543
 R:Drew, J.E.; Bown, D.; Gatehouse, J.A.
 Plant Mol. Biol. 21, 1195-1199, 1993
 A:Title: Sequence of a novel plant ras-related cDNA from Pisum sativum.
 A:Reference number: S33531; MUID:93257636; PMID:8490139
 A:Accession: S33531
 A:Molecule type: mRNA
 A:Residues: 1-206 <DRE>
 A:Cross-references: EMBL:X65650; NID:G20755; PIDN:CAA46600.1; PID:G20756
 A>Note: the authors translated the codon AAA for residue 48 as Thr, and CCC for residue
 C:Genetics:
 A:Gene: rab
 C:Superfamily: ras transforming protein; translation elongation factor Tu homology
 C:Keywords: GTP binding; nucleotide binding; P-loop
 F:9-128/Domain: translation elongation factor Tu homology <ETU>
 F:15-22/Region: nucleotide-binding motif A (P-loop)
 F:125-128/Region: GTP-binding NXXD motif
 F:158-160/Region: GTP-binding SAK/L motif

Query Match 49.2%; Score 523; DB 2; Length 206;
 Best Local Similarity 48.3%; Pred. No. 2.5e-40;
 Matches 97; Conservative 42; Mismatches 58; Indels 4; Gaps 2;

QY 4 KSSLFKVILLGDSGVGKTSIMNQYVQKFTKEYKATIGADFLTKIEVDKDKVTMQIWD 63
 Db 5 RRTLLKVIILGDSGVGKTSIMNQYVQKFTKEYKATIGADFLTKIEVDKDKVTMQIWD 64
 QY 64 AGQERFSLRTPYRGSDCCLLTFSVDDSQFNLNKKKEFIYADVKEPESPFFVILG 123
 Db 65 AGQERFQSLGSAFYRGADCCMLVFDVNNNAKSFDDLDNRDEFILQAGSPDPPNFVVLG 124
 QY 124 NKIDI--SERQVSTEEAQAACRNDGDPYFETSAKDNTNVAAPFEAVRRVLATEDRSD 180
 Db 125 NKIDVGNVRQVTEKKAKAWCAKSGSIPYFETSAKEDINVEAFTCIETNALRNE-EE 183
 QY 181 LIQTDTVNLHRKPKPSSSC 201
 Db 184 ELYLPDITDVGNSSQPRSTGC 204

RESULT 10

T12579
 C:Superfamily: protein Rab7a - common ice plant
 C:Species: Mesembryanthemum crystallinum (common ice plant)
 C>Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 21-Jan-2000
 C:Accession: T12579
 R:Michalowski, C.B.; Bohnert, H.J.
 Submitted to the EMBL Data Library, January 1997
 A:Description: Sequence of a GTP-binding protein from Mesembryanthemum crystallinum.
 A:Reference number: 217539
 A:Accession: T12579
 A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-207 <MIC>
 A:Cross-references: EMBL:U97142; NID:G1842068; PID:G1842069
 C:Superfamily: ras transforming protein; translation elongation factor Tu homology
 C:Keywords: GTP binding; P-loop
 F:9-128/Domain: translation elongation factor Tu homology <BTU>

Query Match 49.0%; Score 520.5; DB 2; Length 207;
 Best Local Similarity 48.5%; Pred. No. 4.2e-40;
 Matches 98; Conservative 41; Mismatches 58; Indels 5; Gaps 3;

QY 4 KSSLFKVILLGDSGVGKTSIMNQYVQKFTKEYKATIGADFLTKIEVDKDKVTMQIWD 63
 Db 5 RRTLLKVIILGDSGVGKTSIMNQYVQKFTKEYKATIGADFLTKIEVDKDKVTMQIWD 64
 QY 64 AGQERFSLRTPYRGSDCCLLTFSVDDSQFNLNKKKEFIYADVKEPESPFFVILG 123
 Db 65 AGQERFQSLGSAFYRGADCCMLVFDVNNNAKSFDDLDNRDEFILQAGSPDPPNFVVLG 124
 QY 124 NKIDI--SERQVSTEEAQAACRNDGDPYFETSAKDNTNVAAPFEAVRRVLATEDRSD 180
 Db 125 NKIDVGNVRQVTEKKAKAWCAKSGSIPYFETSAKEDINVEAFTCIETNALRNE-EE 184
 QY 181 LIQTDTVNLHRKPKP-SSSC 201
 Db 185 TYL-PDTIDMAGSTRPQSSAC 205

RESULT 11

T26119
 C:Superfamily: protein W03C9.3 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000
 C:Accession: T26119
 R:Gregory, J.; Ainscough, R.
 Submitted to the EMBL Data Library, October 1995
 A:Reference number: Z20155
 A:Accession: T26119
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-209 <WIL>
 A:Cross-references: EMBL:Z66516; PIDN:CAA91357.1; GSPDB:GN00020; CESP:W03C9.3
 A:Experimental source: clone W03C9
 C:Genetics:
 A:Gene: CESP.W03C9.3
 A:Map position: 2
 A:Introns: 39/3; 61/3; 112/2; 181/3
 C:Superfamily: ras transforming protein; translation elongation factor Tu homology

Query Match 48.8%; Score 518.5; DB 2; Length 209;
 Best Local Similarity 48.8%; Pred. No. 6.5e-40;
 Matches 101; Conservative 43; Mismatches 56; Indels 7; Gaps 4;

QY 1 MAG--KSSLFKVILLGDSGVGKTSIMNQYVQKFTKEYKATIGADFLTKIEVDKDKVT 58
 Db 1 MSGTRKALLKVIILGDSGVGKTSIMNQYVQKFTKEYKATIGADFLTKIEVDKDKVT 60
 QY 59 QIWDTAGQERFSLRTPYRGSDCCLLTFSVDDSQFNLNKKKEFIYADVKEPESP 118
 Db 61 QIWDTAGQERFQSLGSAFYRGADCCMLVFDVNNNAKSFDDLDNRDEFILQAGSPDPP 120
 QY 119 FVILGNKIDI--SERQVSTEEAQAACRNDGDPYFETSAKDNTNVAAPFEAVRRVLATE 176
 Db 121 FVILGNKVDLESQRAVSSKRAQSWQTKGNIPYFETSAKEDINVEAFTCIETNALRNE 180
 QY 177 -DRSDEHLCQTDVNL--HRKPKPSSSC 200
 Db 181 QETNDFPFPDQIRLNPQNQQNSGC 207

RESULT 12

T03629
 C:Superfamily: protein Rab7b - common tobacco

C;Species: Nicotiana tabacum (common tobacco)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 02-Feb-2001
C;Accession: T03629
R;Haizel, T.; Merkle, T.; Turk, F.; Nagy, F.
Plant Physiol. 108, 59-67, 1995
A;Title: Characterization of membrane-bound small GTP-binding proteins from Nicotiana tabacum
A;Reference number: Z14896; MUID:95303981; PMID:7784525
A;Accession: T03629
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-205 <HAI>
A;Cross-references: EMBL:L29275; NID:G623589; PIDN:AAA74119.1; PID:G623590
A;Experimental source: strain SR1
C;Genetics:
A;Gene: Rab7b
C;Superfamily: ras transforming protein; translation elongation factor Tu homology
C;Keywords: GTP binding; nucleotide binding; P-loop
F;8-127/Domain: translation elongation factor Tu homology <TU>
F;14-21/Region: nucleotide-binding motif A (P-loop)
F;124-127/Region: GTP-binding NKXD motif
F;157-159/Region: GTP-binding SAK/L motif

Query Match 48.5%; Score 515; DB 2; Length 205;
Best Local Similarity 46.6%; Pred. No. 1.3e-39;
Matches 95; Conservative 44; Mismatches 61; Indels 4; Gaps 2;

Qy 1 MAGKSSLFKVLILGDSGVGKSSLMNRYVTKNFTQTLFHTIGVEFLNKDLEVDGHHFTVMOI 60
Db 1 MPSPANLVKVLILGDSGVGKTSLMNQYVNNKFSNQYKATIGADFLTKVEQFEDRLFTLIQI 60

Qy 61 WDTAGQERFSLRTPFYRGSDCLLFTSVDDSOQNLSNWKKEFYIYADVKEPSFPFV 120
Db 61 WDTAGQERFOSLGVAFYRGADCCVLYVDVNSMKSFFENLNWREELIQASPSDPENFPFV 120

Qy 121 ILGNKIDIDGNSRVVSEKKVAKWASKGNIPFETSAKEGTFVDEAFQCIKNAKXSGE 180
Db 121 VLGNKVIDGNSRVVSEKKVAKWASKGNIPFETSAKEGTFVDEAFQCIKNAKXSGE 180

Qy 178 RSDHLIQTDTVNLHKKPKPSSSCC 201
Db 181 -EEIYLPDLDVGTSSQPTGGC 203

RESULT 13
T40425
ras-related protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Jan-2000
C;Accession: T40425
R;Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, March 1999
A;Reference number: Z21928
A;Accession: T40425
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-205 <SEE>
A;Cross-references: EMBL:AL035655; PIDN:CA838603.1; GSPDB:GN00067; SPDB:SPBC405.04C
A;Experimental source: strain 972h-; cosmid c405
C;Genetics:
A;Gene: SPDB:SPBC405.04C
A;Map position: 2
A;Introns: 27/3; 135/3
C;Superfamily: ras transforming protein; translation elongation factor Tu homology

Query Match 48.4%; Score 514; DB 2; Length 205;
Best Local Similarity 47.8%; Pred. No. 1.7e-39;
Matches 97; Conservative 40; Mismatches 62; Indels 4; Gaps 2;

Qy 2 AKKSLFKVILLGDSGVGKSSLMNRYVTKNFTQTLFHTIGVEFLNKDLEVDGHHFTVMOI 61
Db 3 ARREMLKVLILGDSGVGKTSLMNQYVNNKFSNQYKATIGADFLTKVEQFEDRLFTLIQI 62

Qy 62 DTAGQERFSLRTPFYRGSDCLLFTSVDDSOQNLSNWKKEFYIYADVKEPSFPFV 121
Db 63 DTAGQERFOSLGVAFYRGADCCVLYVDVNSMKSFFENLNWREELIQASPSDPENFPFV 122

Qy 122 LGNKIDIDGNSRVVSEKKVAKWASKGNIPFETSAKEGTFVDEAFQCIKNAKXSGE 178
Db 123 LGNKIDIDGNSRVVSEKKVAKWASKGNIPFETSAKEGTFVDEAFQCIKNAKXSGE 181

Qy 179 SDHLIQTDTVNLHKKPKPSSSCC 201
Db 182 EDEIYLPDLDVGTSSQPTGGC 204

RESULT 15
H96562
hypothetical protein F19K6.10 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C;Accession: H96562
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Dewar, T.H.; Dwyer, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

Db 61 LWDTAGQERFOSLGVAFYRGADCCVLYVDVNSKSFETLDSWRDEFLIQASPSNPETFPF 120

Qy 120 VILGNKIDISE--RQVSTEEAQAACRDNDGYPYFETSAKDATNVAAAFEEAVRRVLATED 177

Db 121 ILLGNKVDVEQKENVSKKALACQARGEIPYFETSAKEINVOEAFETVAKALENMD 180

Qy 178 RSDHLIQTDTVNLHKKPKPSSSCC 201

Db 181 SDDIAADFTDPIHLDMSQKTSVCYC 205

RESULT 14
T03628
GTP-binding protein Rab7a - common tobacco
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 02-Feb-2001
C;Accession: T03628
R;Haizel, T.; Merkle, T.; Turk, F.; Nagy, F.
Plant Physiol. 108, 59-67, 1995
A;Title: Characterization of membrane-bound small GTP-binding proteins from Nicotiana tabacum
A;Reference number: Z14896; MUID:95303981; PMID:7784525
A;Accession: T03628
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-206 <HAI>
A;Cross-references: EMBL:L29274; NID:G623587; PIDN:AAA74118.1; PID:G623588
A;Experimental source: strain SR1
C;Genetics:
A;Gene: Rab7a
C;Superfamily: ras transforming protein; translation elongation factor Tu homology
C;Keywords: GTP binding; nucleotide binding; P-loop
F;9-128/Domain: translation elongation factor Tu homology <TU>
F;15-22/Region: nucleotide-binding motif A (P-loop)
F;125-128/Region: GTP-binding NKXD motif
F;158-160/Region: GTP-binding SAK/L motif

Query Match 48.4%; Score 514; DB 2; Length 206;
Best Local Similarity 47.8%; Pred. No. 1.7e-39;
Matches 97; Conservative 40; Mismatches 62; Indels 4; Gaps 2;

Qy 2 AKKSLFKVILLGDSGVGKSSLMNRYVTKNFTQTLFHTIGVEFLNKDLEVDGHHFTVMOI 61
Db 3 ARREMLKVLILGDSGVGKTSLMNQYVNNKFSNQYKATIGADFLTKVEQFEDRLFTLIQI 62

Qy 62 DTAGQERFSLRTPFYRGSDCLLFTSVDDSOQNLSNWKKEFYIYADVKEPSFPFV 121
Db 63 DTAGQERFOSLGVAFYRGADCCVLYVDVNSMKSFFENLNWREELIQASPSDPENFPFV 122

Qy 122 LGNKIDIDGNSRVVSEKKVAKWASKGNIPFETSAKEGTFVDEAFQCIKNAKXSGE 178
Db 123 LGNKIDIDGNSRVVSEKKVAKWASKGNIPFETSAKEGTFVDEAFQCIKNAKXSGE 181

Qy 179 SDHLIQTDTVNLHKKPKPSSSCC 201
Db 182 EDEIYLPDLDVGTSSQPTGGC 204

RESULT 15
H96562
hypothetical protein F19K6.10 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C;Accession: H96562
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Dewar, T.H.; Dwyer, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

Search completed: February 10, 2004, 04:59:00
Job time : 39 secs